

SEQUENCE LISTING

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SUGIYAMA, Yasuo
NISHIDA, Mayumi
TAKETOMI, Shigehisa

<120> Disease Model Animal Carrying Heterologous PPAR Alpha Gene Introduced Thereinto And Use Thereof

<130> 2005-0041A/WMC/00279

<140> 10/521,174

<141> 2005-1-14

<150> JP 2002-206162

<151> 2002-07-15

<160> 9

<170> PatentIn version 3.1

<210> 1

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<212> DNA

<213> Homo sapiens

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<221> CDS

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ggc gat cta gag agc ccg tta tct gaa gag ttc ctg caa gaa atg gga 96
Gly Asp Leu Glu Ser Pro Leu Ser Glu Glu Phe Leu Gln Glu Met Gly
20 25 30
aac atc caa gag att tcg caa tcc atc ggc gag gat agt tct gga agc 144
Asn Ile Gln Glu Ile Ser Gln Ser Ile Gly Glu Asp Ser Ser Gly Ser
35 40 45
ttt ggc ttt acg gaa tac cag tat tta gga agc tgt cct ggc tca gat 192
Phe Gly Phe Thr Glu Tyr Gln Tyr Leu Gly Ser Cys Pro Gly Ser Asp
50 55 60
ggc tcg gtc atc acg gac acg ctt tca cca gct tcg agc ccc tcc tcg 240
Gly Ser Val Ile Thr Asp Thr Leu Ser Pro Ala Ser Ser Pro Ser Ser
65 70 75 80
gtg act tat cct gtg gtc ccc ggc agc gtg gac gag tct ccc agt gga 288
Val Thr Tyr Pro Val Val Pro Gly Ser Val Asp Glu Ser Pro Ser Gly
85 90 95
gca ttg aac atc gaa tgt aga atc tgc ggg gac aag gcc tca ggc tat 336
Ala Leu Asn Ile Glu Cys Arg Ile Cys Gly Asp Lys Ala Ser Gly Tyr
100 105 110
cat tac gga gtc cac gcg tgt gaa ggc tgc aag ggc ttc ttt cgg cga 384
His Tyr Glu Val His Ala Cys Glu Glu Cys Lys Glu Phe Phe Arg Arg
115 120 125
acg att cga ctc aag ctg gtg tat gac aag tgc gac cgc agc tgc aag 432
Thr Ile Arg Leu Lys Leu Val Tyr Asp Lys Cys Asp Arg Ser Cys Lys
130 135 140
atc cag aaa aag aac aga aac aaa tgc cag tat tgt cga ttt cac aag 480
Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe His Lys
145 150 155 160

tgc ctt tct gtc ggg atg tca cac aac gcg att cgt ttt gga cga atg	528
Cys Leu Ser Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met	
165 170 175	
cca aga tct gag aaa gca aaa ctg aaa gca gaa att ctt acc tgt gaa	576
Pro Arg Ser Glu Lys Ala Lys Leu Lys Ala Glu Ile Leu Thr Cys Glu	
180 185 190	
cat gac ata gaa gat tct gaa act gca gat ctc aaa tct ctg gcc aag	624
His Asp Ile Glu Asp Ser Glu Thr Ala Asp Leu Lys Ser Leu Ala Lys	
195 200 205	
aga atc tac gag gcc tac ttg aag aac ttc aac atg aac aag gtc aaa	672
Arg Ile Tyr Glu Ala Tyr Leu Lys Asn Phe Asn Met Asn Lys Val Lys	
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gcc cgg gtc atc ctc tca gga aag gcc agt aac aat cca cct ttt gtc	720
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225 230 235 240	
ata cat gat atg gag aca ctg tgt atg gct gag aag acg ctg gtg gcc	768
Ile His Asp Met Glu Thr Leu Cys Met Ala Glu Lys Thr Leu Val Ala	
245 250 255	
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Lys Leu Val Ala Asn Gly Ile Gln Asn Lys Glu Ala Glu Val Arg Ile	
260 265 270	
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Phe His Cys Cys Gln Cys Thr Ser Val Glu Thr Val Thr Glu Leu Thr	
275 280 285	
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Glu Phe Ala Lys Ala Ile Pro Gly Phe Ala Asn Leu Asp Leu Asn Asp	
290 295 300	
caa gtg aca ttg cta aaa tac gga gtt tat gag gcc ata ttc gcc atg	960
Gln Val Thr Leu Leu Lys Tyr Gly Val Tyr Glu Ala Ile Phe Ala Met	
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ctg tct tct gtg atg aac aaa gac ggg atg ctg gta gcg tat gga aat	1008
Leu Ser Ser Val Met Asn Lys Asp Gly Met Leu Val Ala Tyr Gly Asn	
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Cys Gly Asp Arg Pro Gly Leu Leu Asn Val Gly His Ile Glu Lys Met	
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Gln Glu Gly Ile Val His Val Leu Arg Leu His Leu Gln Ser Asn His	
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Pro Asp Asp Ile Phe Leu Phe Pro Lys Leu Leu Gln Lys Met Ala Asp	
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Leu Arg Gln Leu Val Thr Glu His Ala Gln Leu Val Gln Ile Ile Lys	
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<213> Homo sapiens

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35 40 45
Phe Gly Phe Thr Glu Tyr Gln Tyr Leu Gly Ser Cys Pro Gly Ser Asp
50 55 60
Gly Ser Val Ile Thr Asp Thr Leu Ser Pro Ala Ser Ser Pro Ser Ser
65 70 75 80
Val Thr Tyr Pro Val Val Pro Gly Ser Val Asp Glu Ser Pro Ser Gly
85 90 95
Ala Leu Asn Ile Glu Cys Arg Ile Cys Gly Asp Lys Ala Ser Gly Tyr
100 105 110
His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg
115 120 125
Thr Ile Arg Leu Lys Leu Val Tyr Asp Lys Cys Asp Arg Ser Cys Lys
130 135 140
Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe His Lys
145 150 155 160
Cys Leu Ser Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met
165 170 175
Pro Arg Ser Glu Lys Ala Lys Leu Lys Ala Glu Ile Leu Thr Cys Glu
180 185 190
His Asp Ile Glu Asp Ser Glu Thr Ala Asp Leu Lys Ser Leu Ala Lys
195 200 205
Arg Ile Tyr Glu Ala Tyr Leu Lys Asn Phe Asn Met Asn Lys Val Lys
210 215 220
Ala Arg Val Ile Leu Ser Gly Lys Ala Ser Asn Asn Pro Pro Phe Val
225 230 235 240
Ile His Asp Met Glu Thr Leu Cys Met Ala Glu Lys Thr Leu Val Ala
245 250 255
Lys Leu Val Ala Asn Gly Ile Gln Asn Lys Glu Ala Glu Val Arg Ile
260 265 270
Phe His Cys Cys Gln Cys Thr Ser Val Glu Thr Val Thr Glu Leu Thr
275 280 285
Glu Phe Ala Lys Ala Ile Pro Gly Phe Ala Asn Leu Asp Leu Asn Asp
290 295 300
Gln Val Thr Leu Leu Lys Tyr Gly Val Tyr Glu Ala Ile Phe Ala Met
305 310 315 320
Leu Ser Ser Val Met Asn Lys Asp Gly Met Leu Val Ala Tyr Gly Asn
325 330 335
Gly Phe Ile Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Cys
340 345 350
Asp Ile Met Glu Pro Lys Phe Asp Phe Ala Met Lys Phe Asn Ala Leu
355 360 365
Glu Leu Asp Asp Ser Asp Ile Ser Leu Phe Val Ala Ala Ile Ile Cys
370 375 380
Cys Gly Asp Arg Pro Gly Leu Leu Asn Val Gly His Ile Glu Lys Met
385 390 395 400
Gln Glu Gly Ile Val His Val Leu Arg Leu His Leu Gln Ser Asn His
405 410 415
Pro Asp Asp Ile Phe Leu Phe Pro Lys Leu Leu Gln Lys Met Ala Asp
420 425 430
Leu Arg Gln Leu Val Thr Glu His Ala Gln Leu Val Gln Ile Ile Lys
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detecting human PPAR-alpha cDNA fragment amplified by PCR.

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